Run on: May 9, 2003, 18:24:43 ; Search time 3.72714 Seconds
                                        (without alignments)
                                      1184.134 Million cell updates/sec

Title: US-09-917-383-1

RESULT 2
US-09-917-384-1
; Sequence 1, Application US/09917384
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: ADNEY, WILLIAM S.
; APPLICANT: VINZANT, TODD B.
; APPLICANT: DECKER, STEPHEN R.
; APPLICANT: HIMMEL, MICHAEL E.
; TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
; TITLE OF INVENTION: CELLULOLYTICUS
; FILE REFERENCE: 40170.6US01
; CURRENT APPLICATION NUMBER: US/09/917,384
; CURRENT FILING DATE: 2001-07-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1228
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Segment of
;   OTHER INFORMATION: GuxA
US-09-917-384-1

  Query Match   100.0%; Score 6525; DB 23; Length 1228;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 1228; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MERTQQSGRNCRYQRGTTRMPAISKRLRAGVLAGAVSIAASIVPLAMQHPAIAATHVDNP 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MERTQQSGRNCRYQRGTTRMPAISKRLRAGVLAGAVSIAASIVPLAMQHPAIAATHVDNP 60

Qy   61 YAGATFFVNPYWAQEVQSEAANQTNATLAAKMRVVSTYSTAVWMDRIAAINGVNGGPGLT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YAGATFFVNPYWAQEVQSEAANQTNATLAAKMRVVSTYSTAVWMDRIAAINGVNGGPGLT 120

Qy   121 TYLDAALSQQQGTTPEVIEIVIYDLPGRDCAALASNGELPATAAGLQTYETQYIDPIASI 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TYLDAALSQQQGTTPEVIEIVIYDLPGRDCAALASNGELPATAAGLQTYETQYIDPIASI 180

Qy   181 LSNPKYSSLRIVTIIEPDSLPNAVTNMSIQACATAVPYYEQGIEYALTKLHAIPNVYIYM 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LSNPKYSSLRIVTIIEPDSLPNAVTNMSIQACATAVPYYEQGIEYALTKLHAIPNVYIYM 240

Qy   241 DAAHSGWLGWPNNASGYVQEVQKVLNASIGVNGIDGFVTNTANYTPLKEPFMTATQQVGG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 DAAHSGWLGWPNNASGYVQEVQKVLNASIGVNGIDGFVTNTANYTPLKEPFMTATQQVGG 300

Qy   301 QPVESANFYQWNPDIDEADYAVDLYSRLVAAGFPSSIGMLIDTLRNGWGGPNEPTGPSTA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 QPVESANFYQWNPDIDEADYAVDLYSRLVAAGFPSSIGMLIDTLRNGWGGPNEPTGPSTA 360

Qy   361 TDVNTFVNQSKIDLRQHRGLWCNQNGAGLGQPPQASPTDFPNAHLDAYVWIKPPGESDGT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 TDVNTFVNQSKIDLRQHRGLWCNQNGAGLGQPPQASPTDFPNAHLDAYVWIKPPGESDGT 420

Qy   421 SAASDPTTGKKSDPMCDPTYTTSYGVLTNALPNSPIAGQWFPAQFDQLVANARPAVPTST 480

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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  SAASDPTTGKKSDPMCDPTYTTSYGVLTNALPNSPIAGQWFPAQFDQLVANARPAVPTST  480

Qy     481  SSSPPPPPPSPSASPSPSPSPSSSPSPSPSPSSSPSPSPSPSPSPSSSPSPSPSSSPS  540
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  SSSPPPPPPSPSASPSPSPSPSSSPSPSPSPSSSPSPSPSPSPSPSSSPSPSPSSSPS  540

Qy  (  541  PSPSPSPSPSSSPSPSPSSSPSPSPSPSPSPSSSPSPSPTSSPVSGGLKVQYKNNDSAPG  600
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  PSPSPSPSPSSSPSPSPSSSPSPSPSPSPSPSSSPSPSPTSSPVSGGLKVQYKNNDSAPG  600

Qy     601  DNQIKPGLQLVNTGSSSVDLSTVTVRYWFTRDGGSSTLVYNCDWAAMGCGNIRASFGSVN  660
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  DNQIKPGLQLVNTGSSSVDLSTVTVRYWFTRDGGSSTLVYNCDWAAMGCGNIRASFGSVN  660

Qy     661  PATPTADTYLQLSFTGGTLAAGGSTGEIQNRVNKSDWSNFTETNDYSYGTNTTFQDWTKV  720
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  PATPTADTYLQLSFTGGTLAAGGSTGEIQNRVNKSDWSNFTETNDYSYGTNTTFQDWTKV  720

Qy     721  TVYVNGVLVWGTEPSGTSPSPTPSPSPSPSPSPGGDVTPPSVPTGLVVTGVSGSSVSLAW  780
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  TVYVNGVLVWGTEPSGTSPSPTPSPSPSPSPSPGGDVTPPSVPTGLVVTGVSGSSVSLAW  780

Qy     781  NASTDNVGVAHYNVYRNGVLVGQPTVTSFTDTGLAAGTAYTYTVAAVDAAGNTSAPSTPV  840
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  NASTDNVGVAHYNVYRNGVLVGQPTVTSFTDTGLAAGTAYTYTVAAVDAAGNTSAPSTPV  840

Qy     841  TATTTSPSPSPTPTGTTVTDCTPGPNQNGVTSVQGDEYRVQTNEWNSSAQQCLTINTATG  900
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  TATTTSPSPSPTPTGTTVTDCTPGPNQNGVTSVQGDEYRVQTNEWNSSAQQCLTINTATG  900

Qy     901  AWTVSTANFSGGTGGAPATYPSIYKGCHWGNCTTKNVGMPIQISQIGSAVTSWSTTQVSS  960
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  AWTVSTANFSGGTGGAPATYPSIYKGCHWGNCTTKNVGMPIQISQIGSAVTSWSTTQVSS  960

Qy     961  GAYDVAYDIWTNSTPTTTGQPNGTEIMIWLNSRGGVQPFGSQTATGVTVAGHTWNVWQGQ  1020
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  GAYDVAYDIWTNSTPTTTGQPNGTEIMIWLNSRGGVQPFGSQTATGVTVAGHTWNVWQGQ  1020

Qy    1021  QTSWKIISYVLTPGATSISNLDLKAIFADAAARGSLNTSDYLLDVEAGFEIWQGGQGLGS  1080
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  QTSWKIISYVLTPGATSISNLDLKAIFADAAARGSLNTSDYLLDVEAGFEIWQGGQGLGS  1080

Qy    1081  NSFSVSVTSGTSSPTPSPSPTPTPSPTPTPSPSPTPSPSPTSSPSSSGVACRATYVVNSD  1140
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  NSFSVSVTSGTSSPTPSPSPTPTPSPTPTPSPSPTPSPSPTSSPSSSGVACRATYVVNSD  1140

Qy    1141  WGSGFTATVTVTNTGSRATNGWTVAWSFGGNQTVTNYWNTALTQSGASVTATNLSYNNVI  1200
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  WGSGFTATVTVTNTGSRATNGWTVAWSFGGNQTVTNYWNTALTQSGASVTATNLSYNNVI  1200

Qy    1201  QPGQSTTFGFNGSYSGTNAAPTLSCTAS  1228
                  ||||||||||||||||||||||||||||
Db    1201  QPGQSTTFGFNGSYSGTNAAPTLSCTAS  1228
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RESULT 2
US-09-917-384-2
; Sequence 2, Application US/09917384
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: ADNEY, WILLIAM S.
; APPLICANT: VINZANT, TODD B.
; APPLICANT: DECKER, STEPHEN R.
; APPLICANT: HIMMEL, MICHAEL E.
; TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
; TITLE OF INVENTION: CELLULOLYTICUS
; FILE REFERENCE: 40170.6US01
; CURRENT APPLICATION NUMBER: US/09/917,384
; CURRENT FILING DATE: 2001-07-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 3687
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Segment of
;   OTHER INFORMATION: GuxA
US-09-917-384-2

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  Query Match             100.0%;  Score 3687;  DB 34;  Length 3687;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3687;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 ATGGAGCGAACCCAACAATCCGGACGGAACTGCAGGTACCAGAGAGGAACGACACGAATG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGAGCGAACCCAACAATCCGGACGGAACTGCAGGTACCAGAGAGGAACGACACGAATG 60

Qy     61 CCCGCCATCTCAAAACGGCTGCGAGCCGGCGTCCTCGCCGGGGCGGTGAGCATCGCAGCC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CCCGCCATCTCAAAACGGCTGCGAGCCGGCGTCCTCGCCGGGGCGGTGAGCATCGCAGCC 120

Qy    121 TCCATCGTGCCGCTGGCGATGCAGCATCCTGCCATCGCCGCGACGCACGTCGACAATCCC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TCCATCGTGCCGCTGGCGATGCAGCATCCTGCCATCGCCGCGACGCACGTCGACAATCCC 180

Qy    181 TATGCGGGAGCGACCTTCTTCGTCAACCCGTACTGGGCGCAAGAAGTACAGAGCGAAGCG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TATGCGGGAGCGACCTTCTTCGTCAACCCGTACTGGGCGCAAGAAGTACAGAGCGAAGCG 240

Qy    241 GCGAACCAGACCAATGCCACTCTCGCAGCGAAAATGCGCGTCGTTTCCACATATTCGACG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCGAACCAGACCAATGCCACTCTCGCAGCGAAAATGCGCGTCGTTTCCACATATTCGACG 300

Qy    301 GCCGTCTGGATGGACCGCATCGCTGCGATCAACGGCGTCAACGGCGGACCCGGCTTGACG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCCGTCTGGATGGACCGCATCGCTGCGATCAACGGCGTCAACGGCGGACCCGGCTTGACG 360

Qy    361 ACATATCTGGACGCCGCCCTCTCCCAGCAGCAGGGAACCACCCCTGAAGTCATTGAGATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACATATCTGGACGCCGCCCTCTCCCAGCAGCAGGGAACCACCCCTGAAGTCATTGAGATT 420

Qy    421 GTCATCTACGATCTGCCGGGACGCGACTGCGCGGCGCTCGCCTCCAACGGCGAACTGCCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTCATCTACGATCTGCCGGGACGCGACTGCGCGGCGCTCGCCTCCAACGGCGAACTGCCC 480

Qy    481 GCTACGGCAGCAGGTTTGCAGACCTATGAAACGCAGTACATCGATCCGATTGCGAGTATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GCTACGGCAGCAGGTTTGCAGACCTATGAAACGCAGTACATCGATCCGATTGCGAGTATC 540
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Qy    541 CTGAGCAATCCGAAGTACTCCAGCCTGCGGATCGTGACGATCATTGAGCCGGACTCGCTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGAGCAATCCGAAGTACTCCAGCCTGCGGATCGTGACGATCATTGAGCCGGACTCGCTG 600

Qy    601 CCAAACGCGGTCACCAATATGAGCATTCAAGCGTGTGCAACGGCGGTGCCGTATTACGAG 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CCAAACGCGGTCACCAATATGAGCATTCAAGCGTGTGCAACGGCGGTGCCGTATTACGAG 660

Qy    661 CAAGGCATCGAGTACGCGCTCACGAAATTGCACGCCATTCCGAACGTGTACATCTACATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAAGGCATCGAGTACGCGCTCACGAAATTGCACGCCATTCCGAACGTGTACATCTACATG 720

Qy    721 GACGCCGCCCACTCCGGCTGGCTTGGGTGGCCCAATAATGCCAGCGGATACGTACAGGAA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GACGCCGCCCACTCCGGCTGGCTTGGGTGGCCCAATAATGCCAGCGGATACGTACAGGAA 780

Qy    781 GTCCAGAAGGTCCTCAACGCGAGCATCGGGGTCAACGGCATCGACGGCTTCGTCACCAAC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTCCAGAAGGTCCTCAACGCGAGCATCGGGGTCAACGGCATCGACGGCTTCGTCACCAAC 840

Qy    841 ACGGCGAATTACACGCCGTTGAAGGAGCCGTTCATGACCGCCACCCAGCAGGTCGGCGGA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGGCGAATTACACGCCGTTGAAGGAGCCGTTCATGACCGCCACCCAGCAGGTCGGCGGA 900

Qy    901 CAGCCGGTGGAGTCGGCGAATTTCTACCAGTGGAATCCTGACATCGACGAAGCCGACTAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGCCGGTGGAGTCGGCGAATTTCTACCAGTGGAATCCTGACATCGACGAAGCCGACTAC 960

Qy    961 GCGGTTGACTTGTACTCGCGGCTCGTCGCCGCTGGCTTTCCAAGCAGCATCGGCATGCTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 GCGGTTGACTTGTACTCGCGGCTCGTCGCCGCTGGCTTTCCAAGCAGCATCGGCATGCTC 1020

Qy   1021 ATCGACACCTTACGCAACGGTTGGGGTGGTCCGAACGAACCAACAGGCCCGAGCACCGCG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATCGACACCTTACGCAACGGTTGGGGTGGTCCGAACGAACCAACAGGCCCGAGCACCGCG 1080

Qy   1081 ACCGATGTCAACACCTTCGTCAACCAGTCGAAGATTGACCTTCGGCAGCACCGCGGCCTG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACCGATGTCAACACCTTCGTCAACCAGTCGAAGATTGACCTTCGGCAGCACCGCGGCCTG 1140

Qy   1141 TGGTGCAACCAGAACGGTGCGGGCCTCGGCCAGCCGCCGCAGGCAAGCCCGACGGACTTC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TGGTGCAACCAGAACGGTGCGGGCCTCGGCCAGCCGCCGCAGGCAAGCCCGACGGACTTC 1200

Qy   1201 CCGAACGCGCACCTCGACGCGTATGTCTGGATCAAGCCGCCGGGTGAGTCGGACGGCACA 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CCGAACGCGCACCTCGACGCGTATGTCTGGATCAAGCCGCCGGGTGAGTCGGACGGCACA 1260

Qy   1261 AGCGCTGCGAGCGATCCGACAACTGGCAAGAAGTCGGACCCCATGTGCGACCCGACGTAC 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AGCGCTGCGAGCGATCCGACAACTGGCAAGAAGTCGGACCCCATGTGCGACCCGACGTAC 1320

Qy   1321 ACGACGTCGTACGGGGTACTGACCAACGCGTTACCGAACTCCCCGATCGCCGGCCAGTGG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ACGACGTCGTACGGGGTACTGACCAACGCGTTACCGAACTCCCCGATCGCCGGCCAGTGG 1380

Qy   1381 TTCCCGGCGCAGTTTGACCAGCTTGTCGCGAACGCACGGCCAGCGGTGCCGACGTCGACC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTCCCGGCGCAGTTTGACCAGCTTGTCGCGAACGCACGGCCAGCGGTGCCGACGTCGACC 1440

Qy   1441 AGCTCGAGCCCGCCGCCTCCGCCGCCGAGTCCGTCGGCTTCGCCGAGTCCGAGCCCGAGT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 AGCTCGAGCCCGCCGCCTCCGCCGCCGAGTCCGTCGGCTTCGCCGAGTCCGAGCCCGAGT 1500

Qy   1501 CCGAGCCCGAGCAGCTCGCCATCGCCGTCGCCGTCTCCGAGCTCGAGCCCGTCTCCGTCG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CCGAGCCCGAGCAGCTCGCCATCGCCGTCGCCGTCTCCGAGCTCGAGCCCGTCTCCGTCG 1560
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Qy   1561 CCGAGCCCGAGTCCGAGCCCGAGTAGCTCGCCGTCGCCGTCTCCGAGCTCGAGCCCGTCT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CCGAGCCCGAGTCCGAGCCCGAGTAGCTCGCCGTCGCCGTCTCCGAGCTCGAGCCCGTCT 1620

Qy   1621 CCGTCGCCGAGCCCGAGTCCGAGCCCGAGTAGCTCGCCGTCGCCGTCTCCGAGCTCGAGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCGTCGCCGAGCCCGAGTCCGAGCCCGAGTAGCTCGCCGTCGCCGTCTCCGAGCTCGAGC 1680

Qy   1681 CCGTCTCCGTCGCCGAGCCCGAGTCCGAGCCCGAGTAGCTCGCCGTCGCCGTCTCCGACG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CCGTCTCCGTCGCCGAGCCCGAGTCCGAGCCCGAGTAGCTCGCCGTCGCCGTCTCCGACG 1740

Qy   1741 TCGTCGCCGGTGTCGGGTGGGCTGAAGGTGCAGTACAAGAACAATGATTCGGCGCCGGGT 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 TCGTCGCCGGTGTCGGGTGGGCTGAAGGTGCAGTACAAGAACAATGATTCGGCGCCGGGT 1800

Qy   1801 GATAACCAGATCAAACCGGGTCTCCAGTTGGTGAATACCGGGTCGTCGTCGGTGGATTTG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GATAACCAGATCAAACCGGGTCTCCAGTTGGTGAATACCGGGTCGTCGTCGGTGGATTTG 1860

Qy   1861 TCGACGGTGACGGTGCGGTACTGGTTCACCCGGGATGGTGGGTCGTCGACACTGGTGTAC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TCGACGGTGACGGTGCGGTACTGGTTCACCCGGGATGGTGGGTCGTCGACACTGGTGTAC 1920

Qy   1921 AACTGTGACTGGGCGGCGATGGGGTGTGGGAATATCCGCGCCTCGTTCGGCTCGGTGAAC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 AACTGTGACTGGGCGGCGATGGGGTGTGGGAATATCCGCGCCTCGTTCGGCTCGGTGAAC 1980

Qy   1981 CCGGCGACGCCGACGGCGGACACCTACCTGCAGTTGTCGTTCACTGGTGGAACGTTGGCC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CCGGCGACGCCGACGGCGGACACCTACCTGCAGTTGTCGTTCACTGGTGGAACGTTGGCC 2040

Qy   2041 GCTGGTGGGTCGACGGGTGAGATTCAAAACCGGGTGAATAAGAGTGACTGGTCGAATTTC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCTGGTGGGTCGACGGGTGAGATTCAAAACCGGGTGAATAAGAGTGACTGGTCGAATTTC 2100

Qy   2101 ACCGAGACCAATGACTACTCGTATGGGACGAACACCACCTTCCAGGACTGGACGAAGGTG 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 ACCGAGACCAATGACTACTCGTATGGGACGAACACCACCTTCCAGGACTGGACGAAGGTG 2160

Qy   2161 ACGGTGTACGTCAACGGCGTGTTGGTGTGGGGGACTGAACCGTCCGGCACCAGCCCCAGC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 ACGGTGTACGTCAACGGCGTGTTGGTGTGGGGGACTGAACCGTCCGGCACCAGCCCCAGC 2220

Qy   2221 CCCACACCATCCCCGAGCCCGAGCCCGAGCCCGAGCCCGGGTGGGGATGTGACGCCGCCG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCCACACCATCCCCGAGCCCGAGCCCGAGCCCGAGCCCGGGTGGGGATGTGACGCCGCCG 2280

Qy   2281 AGTGTGCCGACCGGCTTGGTGGTGACGGGGGTGAGTGGGTCGTCGGTGTCGTTGGCGTGG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGTGTGCCGACCGGCTTGGTGGTGACGGGGGTGAGTGGGTCGTCGGTGTCGTTGGCGTGG 2340

Qy   2341 AATGCGTCGACGGATAACGTGGGGGTGGCGCATTACAACGTGTACCGCAACGGGGTGTTG 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AATGCGTCGACGGATAACGTGGGGGTGGCGCATTACAACGTGTACCGCAACGGGGTGTTG 2400

Qy   2401 GTGGGCCAGCCGACGGTGACCTCGTTCACCGACACGGGTTTGGCCGCGGGAACCGCGTAC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GTGGGCCAGCCGACGGTGACCTCGTTCACCGACACGGGTTTGGCCGCGGGAACCGCGTAC 2460

Qy   2461 ACCTACACGGTGGCCGCGGTGGACGCTGCGGGTAACACCTCCGCCCCATCCACCCCCGTC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 ACCTACACGGTGGCCGCGGTGGACGCTGCGGGTAACACCTCCGCCCCATCCACCCCCGTC 2520

Qy   2521 ACCGCCACCACCACGAGTCCCAGCCCCAGCCCCACGCCGACGGGGACCACGGTCACCGAC 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2521 ACCGCCACCACCACGAGTCCCAGCCCCAGCCCCACGCCGACGGGGACCACGGTCACCGAC 2580

Qy    2581 TGCACGCCCGGTCCTAACCAGAATGGTGTGACCAGCGTGCAGGGCGACGAATACCGGGTG 2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 TGCACGCCCGGTCCTAACCAGAATGGTGTGACCAGCGTGCAGGGCGACGAATACCGGGTG 2640

Qy    2641 CAGACCAATGAGTGGAATTCGTCGGCCCAGCAGTGCCTCACCATCAATACCGCGACCGGT 2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 CAGACCAATGAGTGGAATTCGTCGGCCCAGCAGTGCCTCACCATCAATACCGCGACCGGT 2700

Qy    2701 GCCTGGACGGTGAGCACTGCGAACTTCAGCGGTGGGACCGGCGGTGCGCCCGCGACGTAT 2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 GCCTGGACGGTGAGCACTGCGAACTTCAGCGGTGGGACCGGCGGTGCGCCCGCGACGTAT 2760

Qy    2761 CCGTCGATCTACAAGGGCTGCCACTGGGGCAACTGCACCACGAAGAACGTCGGGATGCCG 2820
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 CCGTCGATCTACAAGGGCTGCCACTGGGGCAACTGCACCACGAAGAACGTCGGGATGCCG 2820

Qy    2821 ATTCAGATCAGTCAGATTGGTTCGGCTGTGACGTCGTGGAGTACGACGCAGGTGTCGTCG 2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 ATTCAGATCAGTCAGATTGGTTCGGCTGTGACGTCGTGGAGTACGACGCAGGTGTCGTCG 2880

Qy    2881 GGCGCGTATGACGTGGCCTACGACATTTGGACGAACAGTACCCCAACGACAACCGGTCAG 2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 GGCGCGTATGACGTGGCCTACGACATTTGGACGAACAGTACCCCAACGACAACCGGTCAG 2940

Qy    2941 CCAAACGGTACCGAAATCATGATTTGGCTGAATTCGCGTGGTGGGGTGCAGCCGTTCGGG 3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 CCAAACGGTACCGAAATCATGATTTGGCTGAATTCGCGTGGTGGGGTGCAGCCGTTCGGG 3000

Qy    3001 TCGCAGACAGCGACGGGTGTGACGGTCGCTGGTCACACGTGGAATGTCTGGCAGGGTCAG 3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||.||||||||
Db    3001 TCGCAGACAGCGACGGGTGTGACGGTCGCTGGTCACACGTGGAATGTCTGGCAGGGTCAG 3060

Qy    3061 CAGACCTCGTGGAAGATTATTTCCTACGTCCTGACCCCCGGTGCGACGTCGATCAGTAAT 3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 CAGACCTCGTGGAAGATTATTTCCTACGTCCTGACCCCCGGTGCGACGTCGATCAGTAAT 3120

Qy    3121 CTGGATTTGAAGGCGATTTTCGCGGACGCCGCGGCACGCGGGTCGCTCAACACCTCCGAT 3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121 CTGGATTTGAAGGCGATTTTCGCGGACGCCGCGGCACGCGGGTCGCTCAACACCTCCGAT 3180

Qy    3181 TACCTGCTCGACGTTGAGGCCGGGTTTGAGATCTGGCAAGGTGGTCAGGGCCTGGGCAGC 3240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181 TACCTGCTCGACGTTGAGGCCGGGTTTGAGATCTGGCAAGGTGGTCAGGGCCTGGGCAGC 3240

Qy    3241 AACTCGTTCAGCGTCTCCGTGACGAGCGGCACGTCCAGCCCGACACCGAGCCCGAGCCCG 3300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3241 AACTCGTTCAGCGTCTCCGTGACGAGCGGCACGTCCAGCCCGACACCGAGCCCGAGCCCG 3300

Qy    3301 ACGCCGACACCGAGCCCGACGCCGACACCGTCTCCGAGCCCGACCCCGTCGCCGAGTCCG 3360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 ACGCCGACACCGAGCCCGACGCCGACACCGTCTCCGAGCCCGACCCCGTCGCCGAGTCCG 3360

Qy    3361 ACCAGCTCGCCGTCGTCGTCGGGTGTGGCGTGCCGGGCGACGTATGTGGTGAATAGTGAT 3420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||.|||
Db    3361 ACCAGCTCGCCGTCGTCGTCGGGTGTGGCGTGCCGGGCGACGTATGTGGTGAATAGTGAT 3420

Qy    3421 TGGGGTTCTGGGTTTACGGCGACGGTGACGGTGACGAATACCGGGAGCCGGGCGACGAAC 3480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 TGGGGTTCTGGGTTTACGGCGACGGTGACGGTGACGAATACCGGGAGCCGGGCGACGAAC 3480

Qy    3481 GGGTGGACGGTGGCGTGGTCGTTTGGTGGGAATCAGACGGTCACGAACTACTGGAACACT 3540
           ||||||||.|||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 GGGTGGACGGTGGCGTGGTCGTTTGGTGGGAATCAGACGGTCACGAACTACTGGAACACT 3540

Qy    3541 GCGTTGACCCAATCAGGTGCATCGGTGACGGCGACGAACCTGAGTTACAACAACGTGATC 3600
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     •           ⌐       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541  GCGTTGACCCAATCAGGTGCATCGGTGACGGCGACGAACCTGAGTTACAACAACGTGATC  3600

Qy   3601  CAACCGGGTCAGTCGACCACCTTCGGATTCAACGGAAGTTACTCAGGAACAAACGCCGCG  3660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601  CAACCGGGTCAGTCGACCACCTTCGGATTCAACGGAAGTTACTCAGGAACAAACGCCGCG  3660

Qy   3661  CCGACGCTCAGCTGCACAGCCAGCTGA  3687
           |||||||||||||||||||||||||||
Db   3661  CCGACGCTCAGCTGCACAGCCAGCTGA  3687
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RESULT 3
US-09-917-384-4
; Sequence 4, Application US/09917384
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: ADNEY, WILLIAM S.
; APPLICANT: VINZANT, TODD B.
; APPLICANT: DECKER, STEPHEN R.
; APPLICANT: HIMMEL, MICHAEL E.
; TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
; TITLE OF INVENTION: CELLULOLYTICUS
; FILE REFERENCE: 40170.6US01
; CURRENT APPLICATION NUMBER: US/09/917,384
; CURRENT FILING DATE: 2001-07-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 423
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Segment of
;   OTHER INFORMATION: GuxA
US-09-917-384-4

    Query Match   100.0%;   Score 2249; DB 23;   Length 423;
    Best Local Similarity   100.0%;   Pred. No. 6.3e-209;
    Matches 423; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ATHVDNPYAGATFFVNPYWAQEVQSEAANQTNATLAAKMRVVSTYSTAVWMDRIAAINGV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATHVDNPYAGATFFVNPYWAQEVQSEAANQTNATLAAKMRVVSTYSTAVWMDRIAAINGV 60

Qy   61 NGGPGLTTYLDAALSQQQGTTPEVIEIVIYDLPGRDCAALASNGELPATAAGLQTYETQY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 NGGPGLTTYLDAALSQQQGTTPEVIEIVIYDLPGRDCAALASNGELPATAAGLQTYETQY 120

Qy   121 IDPIASILSNPKYSSLRIVTIIEPDSLPNAVTNMSIQACATAVPYYEQGIEYALTKLHAI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 IDPIASILSNPKYSSLRIVTIIEPDSLPNAVTNMSIQACATAVPYYEQGIEYALTKLHAI 180

Qy   181 PNVYIYMDAAHSGWLGWPNNASGYVQEVQKVLNASIGVNGIDGFVTNTANYTPLKEPFMT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 PNVYIYMDAAHSGWLGWPNNASGYVQEVQKVLNASIGVNGIDGFVTNTANYTPLKEPFMT 240

Qy   241 ATQQVGGQPVESANFYQWNPDIDEADYAVDLYSRLVAAGFPSSIGMLIDTLRNGWGGPNE 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 ATQQVGGQPVESANFYQWNPDIDEADYAVDLYSRLVAAGFPSSIGMLIDTLRNGWGGPNE 300

Qy   301 PTGPSTATDVNTFVNQSKIDLRQHRGLWCNQNGAGLGQPPQASPTDFPNAHLDAYVWIKP 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 PTGPSTATDVNTFVNQSKIDLRQHRGLWCNQNGAGLGQPPQASPTDFPNAHLDAYVWIKP 360

Qy   361 PGESDGTSAASDPTTGKKSDPMCDPTYTTSYGVLTNALPNSPIAGQWFPAQFDQLVANAR 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 PGESDGTSAASDPTTGKKSDPMCDPTYTTSYGVLTNALPNSPIAGQWFPAQFDQLVANAR 420

Qy   421 PAV 423
          |||
Db   421 PAV 423

RESULT 2
US-09-917-384-5
; Sequence 5, Application US/09917384
; GENERAL INFORMATION:
;   APPLICANT: DING, SHI-YOU
;   APPLICANT: ADNEY, WILLIAM S.
;   APPLICANT: VINZANT, TODD B.
;   APPLICANT: DECKER, STEPHEN R.
;   APPLICANT: HIMMEL, MICHAEL E.
;   TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
;   TITLE OF INVENTION: CELLULOLYTICUS
;   FILE REFERENCE: 40170.6US01
;   CURRENT APPLICATION NUMBER: US/09/917,384
;   CURRENT FILING DATE: 2001-07-28
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 150
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Segment of
;   OTHER INFORMATION: GuxA
US-09-917-384-5

  Query Match   100.0%;   Score 806;   DB 23;   Length 150;
  Best Local Similarity   100.0%;   Pred. No. 3.2e-80;
  Matches   150;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy      1 VSGGLKVQYKNNDSAPGDNQIKPGLQLVNTGSSSVDLSTVTVRYWFTRDGGSSTLVYNCD 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 VSGGLKVQYKNNDSAPGDNQIKPGLQLVNTGSSSVDLSTVTVRYWFTRDGGSSTLVYNCD 60

Qy     61 WAAMGCGNIRASFGSVNPATPTADTYLQLSFTGGTLAAGGSTGEIQNRVNKSDWSNFTET 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 WAAMGCGNIRASFGSVNPATPTADTYLQLSFTGGTLAAGGSTGEIQNRVNKSDWSNFTET 120

Qy    121 NDYSYGTNTTFQDWTKVTVYVNGVLVWGTE 150
          ||||||||||||||||||||||||||||||
Db    121 NDYSYGTNTTFQDWTKVTVYVNGVLVWGTE 150
```

RESULT 2
US-09-917-384-7
; Sequence 7, Application US/09917384
; GENERAL INFORMATION:
;   APPLICANT: DING, SHI-YOU
;   APPLICANT: ADNEY, WILLIAM S.
;   APPLICANT: VINZANT, TODD B.
;   APPLICANT: DECKER, STEPHEN R.
;   APPLICANT: HIMMEL, MICHAEL E.
;   TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
;   TITLE OF INVENTION: CELLULOLYTICUS
;   FILE REFERENCE: 40170.6US01
;   CURRENT APPLICATION NUMBER: US/09/917,384
;   CURRENT FILING DATE: 2001-07-28
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 231
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Segment of
;   OTHER INFORMATION: GuxA
US-09-917-384-7

    Query Match   100.0%;   Score 1244; DB 23;   Length 231;
    Best Local Similarity   100.0%;   Pred. No. 1.3e-115;
    Matches 231; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 DCTPGPNQNGVTSVQDGEYRVQTNEWNSSAQQCLTINTATGAWTVSTANFSGGTGGAPAT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DCTPGPNQNGVTSVQDGEYRVQTNEWNSSAQQCLTINTATGAWTVSTANFSGGTGGAPAT 60

Qy   61 YPSIYKGCHWGNCTTKNVGMPIQISQIGSAVTSWSTTQVSSGAYDVAYDIWTNSTPTTTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 YPSIYKGCHWGNCTTKNVGMPIQISQIGSAVTSWSTTQVSSGAYDVAYDIWTNSTPTTTG 120

Qy   121 QPNGTEIMIWLNSRGGVQPFGSQTATGVTVAGHTWNVWQGQQTSWKIISYVLTPGATSIS 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 QPNGTEIMIWLNSRGGVQPFGSQTATGVTVAGHTWNVWQGQQTSWKIISYVLTPGATSIS 180

Qy   181 NLDLKAIFADAAARGSLNTSDYLLDVEAGFEIWQGGQGLGSNSFSVSVTSG 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 NLDLKAIFADAAARGSLNTSDYLLDVEAGFEIWQGGQGLGSNSFSVSVTSG 231

RESULT 2
US-09-917-384-8
; Sequence 8, Application US/09917384
; GENERAL INFORMATION:
; APPLICANT: DING, SHI-YOU
; APPLICANT: ADNEY, WILLIAM S.
; APPLICANT: VINZANT, TODD B.
; APPLICANT: DECKER, STEPHEN R.
; APPLICANT: HIMMEL, MICHAEL E.
; TITLE OF INVENTION: THERMAL TOLERANT CELLULASE FROM ACIDOTHERMUS
; TITLE OF INVENTION: CELLULOLYTICUS
; FILE REFERENCE: 40170.6US01
; CURRENT APPLICATION NUMBER: US/09/917,384
; CURRENT FILING DATE: 2001-07-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 101
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Segment of
;   OTHER INFORMATION: GuxA
US-09-917-384-8

   Query Match   100.0%; Score 541; DB 23; Length 101;
   Best Local Similarity 100.0%; Pred. No. 1.3e-51;
   Matches 101; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GVACRATYVVNSDWGSGFTATVTVTNTGSRATNGWTVAWSFGGNQTVTNYWNTALTQSGA 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GVACRATYVVNSDWGSGFTATVTVTNTGSRATNGWTVAWSFGGNQTVTNYWNTALTQSGA 60

Qy   61 SVTATNLYSNNVIQPGQSTTFGFNGSYSGTNAAPTLSCTAS 101
          |||||||||||||||||||||||||||||||||||||||||
Db   61 SVTATNLYSNNVIQPGQSTTFGFNGSYSGTNAAPTLSCTAS 101